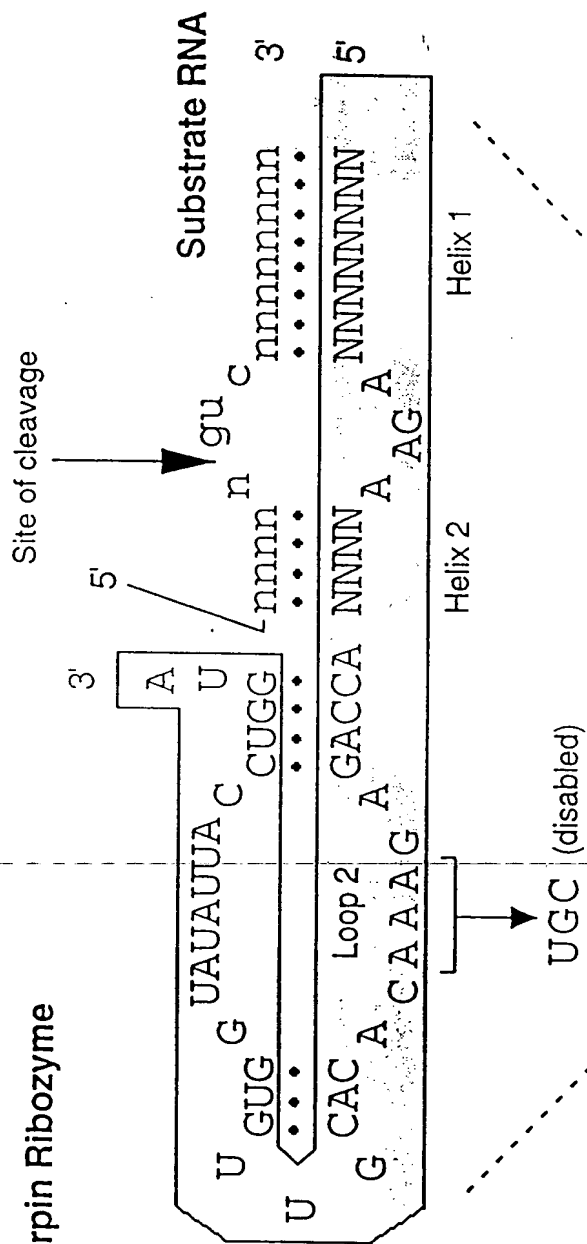
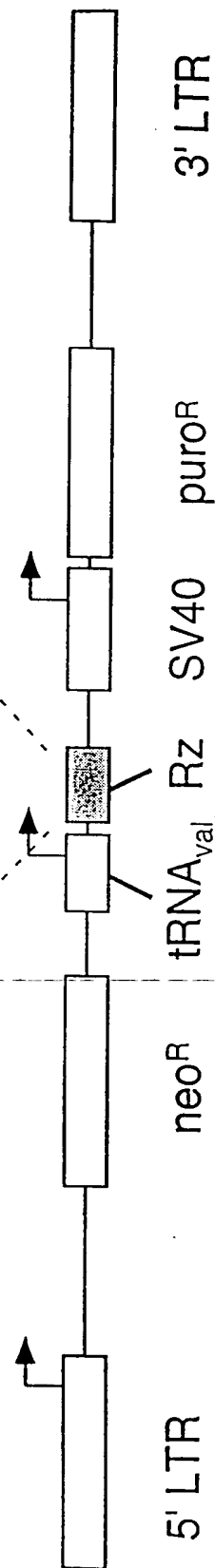


A. Randomized Hairpin Ribozyme



B. Ribozyme Library Vector





Hela

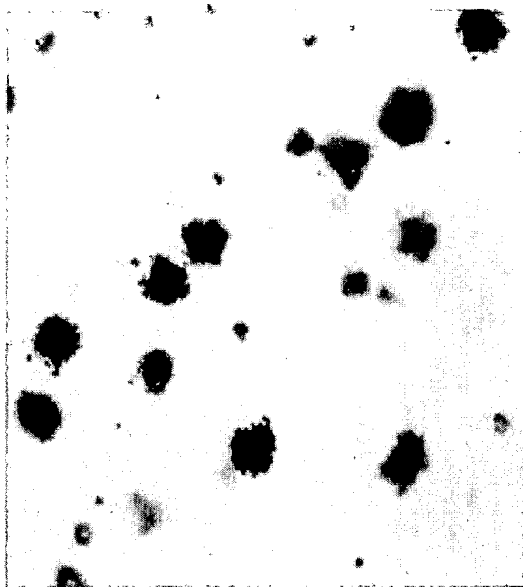


Fig. 2A

HF

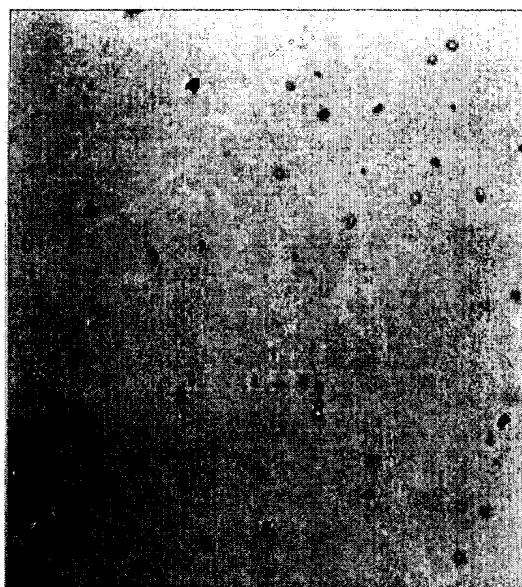


Fig. 2B

HF-568

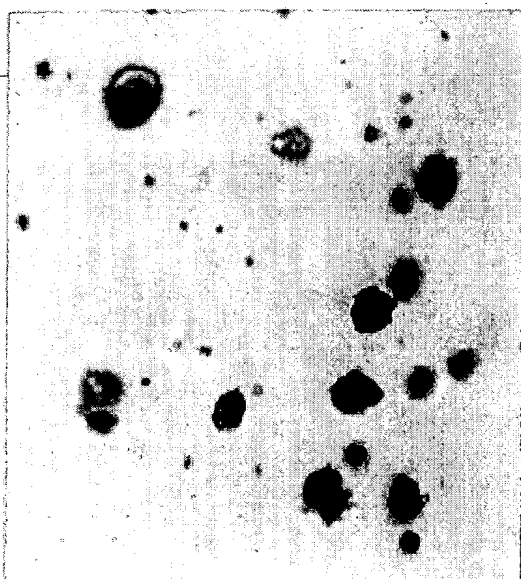


Fig. 2C

HF-d568

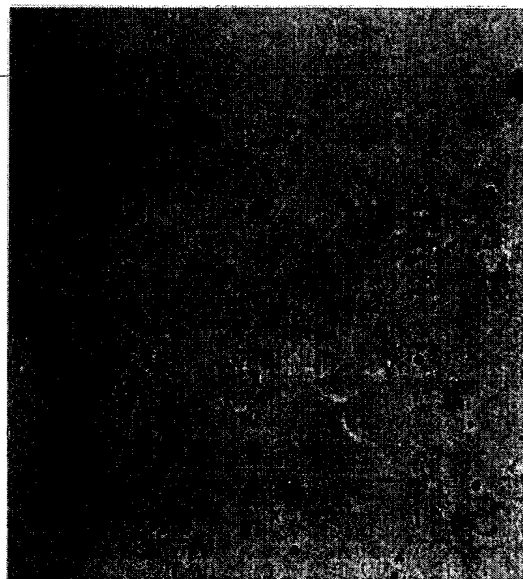
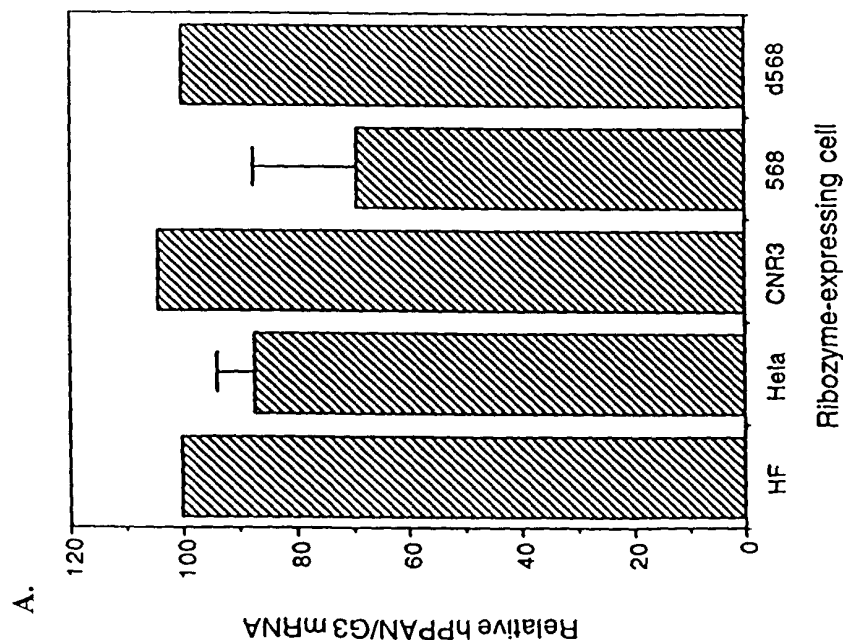


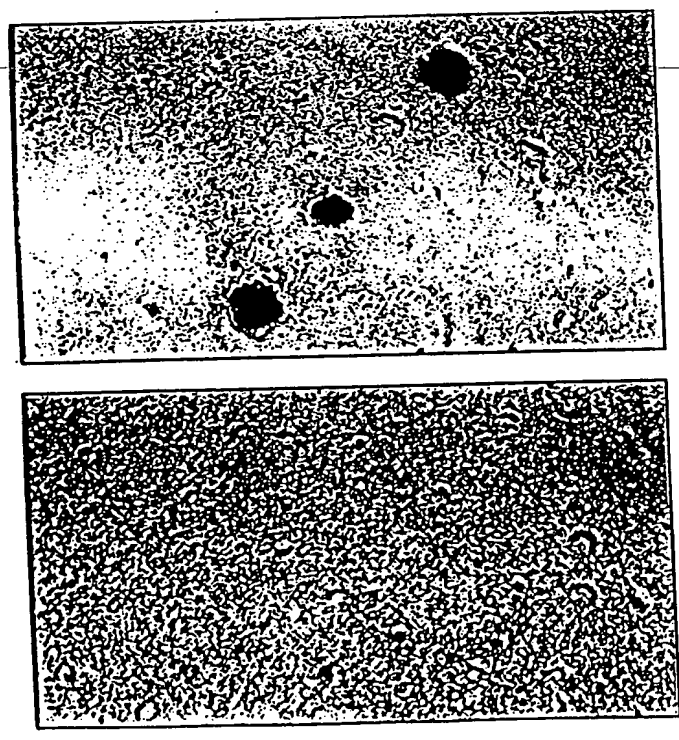
Fig. 2D

B.

Hs	50	WQSGSRHQ	KRAPPQQLR	NDAVAMPH	SVFTRCTG	AVFQSLDV
Nm	50	WQSGSRHQ	KRPPQQLR	NDAVAMPH	SVFTRCTG	AVFQSLDV
Dm	49	WQSGSRHQ	KRPPQQLR	NDAVAMPH	SVFTRCTG	AVFQSLDV
Hs	100	RRMEHVTAS	RLOVRKNSL	KDCVAVAGPL	SVTHFATIA	QELNMEKLM
Nm	100	RRMEHVTAS	RLOVRKNSL	KDCVAVAGPL	SVTHFATIA	QELNMEKLM
Dm	99	RRMEHVTAS	RLOVRKNSL	KDCVAVAGPL	SVTHFATIA	QELNMEKLM
Hs	150	RLGGPTLTF	QSKVTLTD	WSSRRHRM	FEQQAHPPL	AVANSTGHG
Nm	150	RLGGPTLTF	QSKVTLTD	WSSRRHRM	FEQQAHPPL	AVANSTGHG
Dm	149	RLGGPTLTF	QSKVTLTD	WSSRRHRM	FEQQAHPPL	AVANSTGHG
Hs	200	WVVGSRGV	KLLQKQFN	SRLODISEL	LVNLTIRRC	ELDRHYSLR
Nm	200	WVVGSRGV	KLLQKQFN	SRLODISEL	LVNLTIRRC	ELDRHYSLR
Dm	199	WVVGSRGV	KLLQKQFN	SRLODISEL	LVNLTIRRC	ELDRHYSLR
Hs	250	WVVGSRGV	KLLQKQFN	SRLODISEL	LVNLTIRRC	ELDRHYSLR
Nm	250	WVVGSRGV	KLLQKQFN	SRLODISEL	LVNLTIRRC	ELDRHYSLR
Dm	249	WVVGSRGV	KLLQKQFN	SRLODISEL	LVNLTIRRC	ELDRHYSLR
Hs	300	WVVGSRGV	KLLQKQFN	SRLODISEL	LVNLTIRRC	ELDRHYSLR
Nm	300	WVVGSRGV	KLLQKQFN	SRLODISEL	LVNLTIRRC	ELDRHYSLR
Dm	298	WVVGSRGV	KLLQKQFN	SRLODISEL	LVNLTIRRC	ELDRHYSLR
Hs	350	WVVGSRGV	KLLQKQFN	SRLODISEL	LVNLTIRRC	ELDRHYSLR
Nm	348	WVVGSRGV	KLLQKQFN	SRLODISEL	LVNLTIRRC	ELDRHYSLR
Dm	348	WVVGSRGV	KLLQKQFN	SRLODISEL	LVNLTIRRC	ELDRHYSLR
Hs	399	WVVGSRGV	KLLQKQFN	SRLODISEL	LVNLTIRRC	ELDRHYSLR
Nm	398	WVVGSRGV	KLLQKQFN	SRLODISEL	LVNLTIRRC	ELDRHYSLR
Dm	373	WVVGSRGV	KLLQKQFN	SRLODISEL	LVNLTIRRC	ELDRHYSLR
Hs	439	WVVGSRGV	KLLQKQFN	SRLODISEL	LVNLTIRRC	ELDRHYSLR
Nm	437	WVVGSRGV	KLLQKQFN	SRLODISEL	LVNLTIRRC	ELDRHYSLR
Dm	423	WVVGSRGV	KLLQKQFN	SRLODISEL	LVNLTIRRC	ELDRHYSLR
Hs	473	WVVGSRGV	KLLQKQFN	SRLODISEL	LVNLTIRRC	ELDRHYSLR
Dm	460	WVVGSRGV	KLLQKQFN	SRLODISEL	LVNLTIRRC	ELDRHYSLR

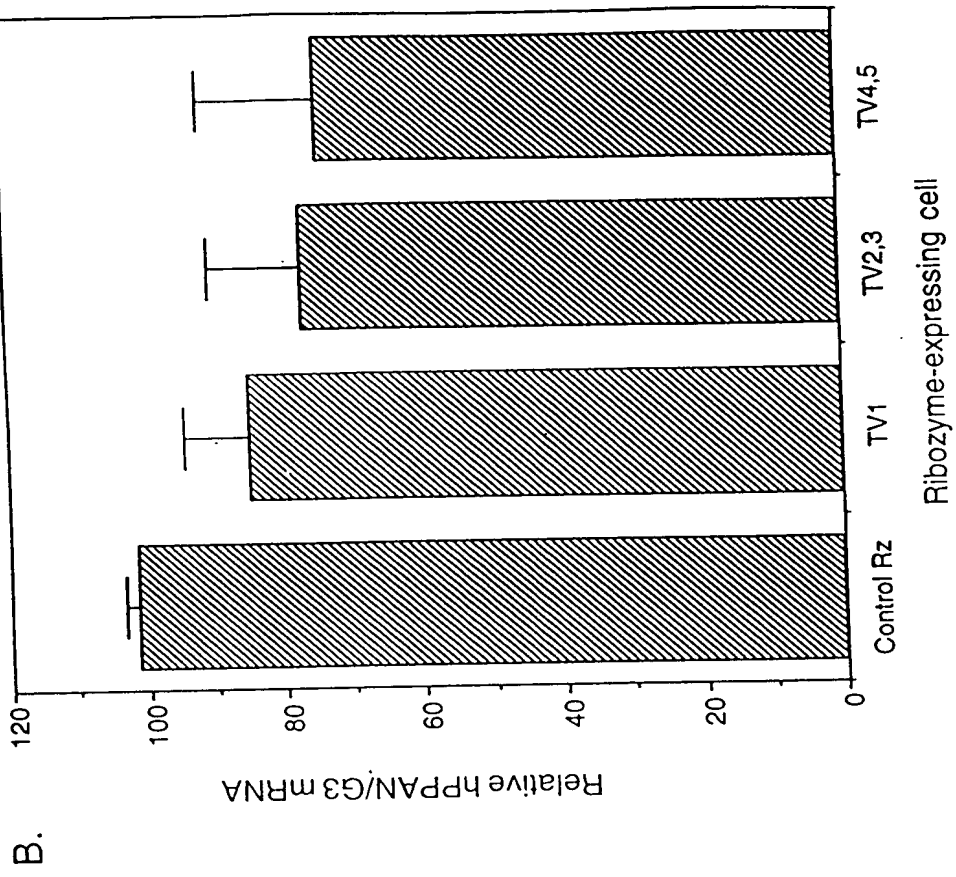
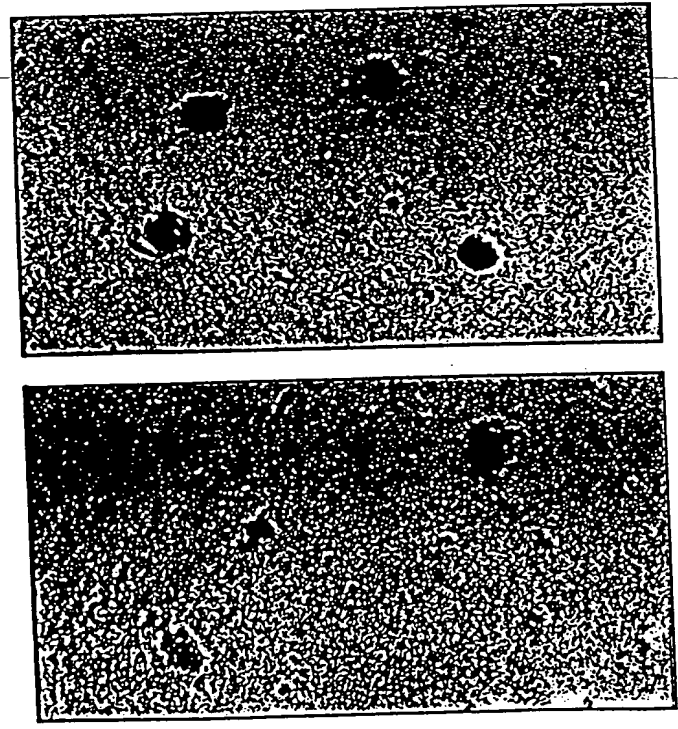


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TV1

Control Rz





HF

HeLa

Vector

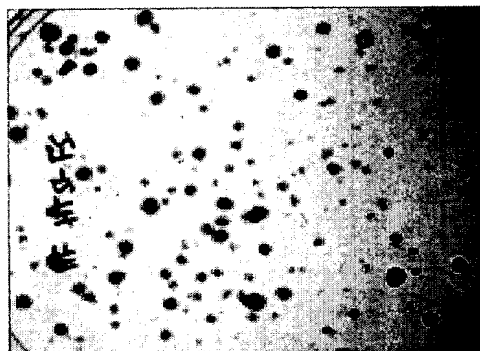


Fig. 5A

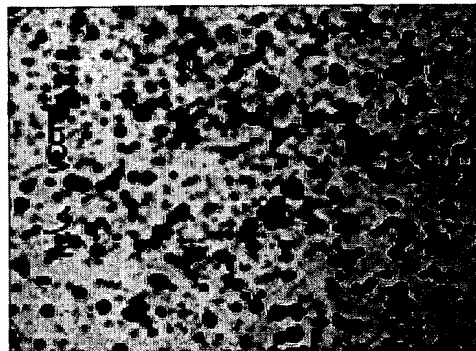


Fig. 5B

hPPAN

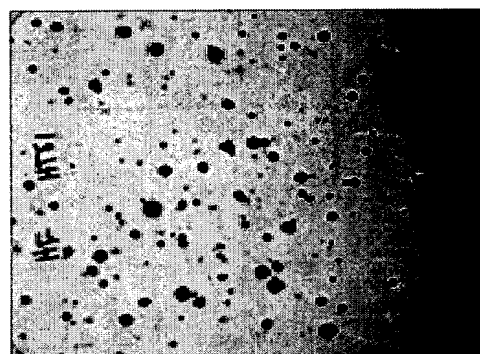


Fig. 5C

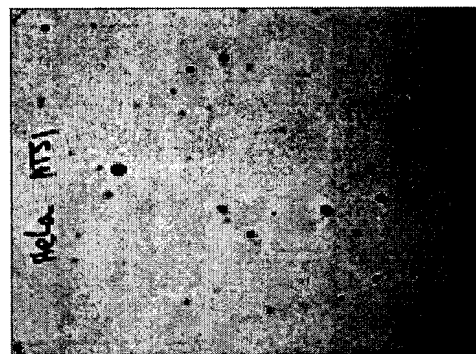


Fig. 5D

FS

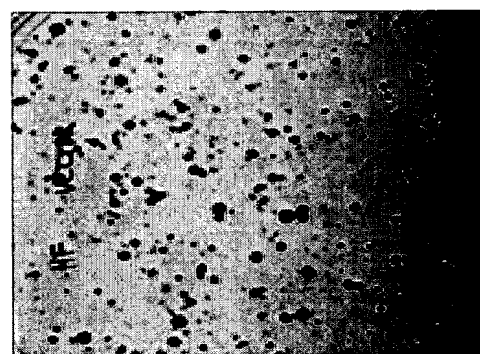


Fig. 5E

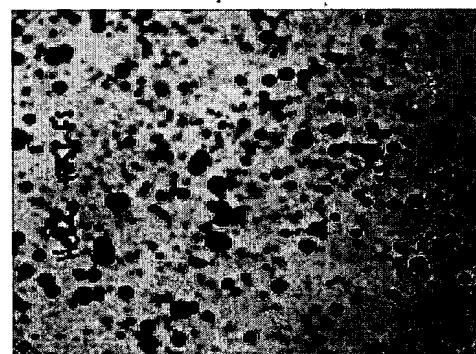


Fig. 5F

	10	20	30	40	50	60
1	GCCTGATGTC	GTCCACAGCC	GTGCCGGCTC	TCAGGCGCCG	GAAGTGAGCT	GCGCACGGCC 60
61	GGAAGCGGCG	GACGCAGGAG	GCCTCGTGGA	GGACACAGCA	GCATGGGACA	GTCAGGGAGG 120
121	TCCCGGCACC	AGAAGCGCGC	CCCGCCCCAG	GCGCAGCTCC	GCAACCTCGA	GGCCTATGCC 180
181	GCGAACCOCG	ACTCGTTCTG	GTTACGCGCA	GGCTGCACGG	GTCCCAACAT	CCGGCAGCTC 240
241	AGCCTGGACG	TGCGCGCGGT	CATGGAGCCC	GTCAC TGCCA	GCGCTCTGCA	GGTTCTGTAA 300
301	AAGAACTCGC	TGAAGGACTG	CGTGGCAGTG	GCTGGGCCCC	TCGGGTTCAC	ACACTTTCTG 360
361	ATCTTAGCAA	AACAAGAGAC	CAATGTCTAC	TTTAAGCTGA	TGCGCTCCC	AGGAGGCCCC 420
421	ACCTTGACCT	TCCAGGTCAA	GAAGTACTCG	CTGGTGCGTG	ATGTGGTCTC	CTCACTGCGC 480
481	CGGCACCGCA	TGCACGAGCA	GCAGTTTGCC	CACCCACCCC	TCCTGGTACT	CAACAGCTTT 540
541	GGCCCCCATG	GTATGCATGT	GAAGCTCATG	GCCACCATGT	TCCAGAACCT	GTTCCCTCC 600
601	ATCAACGTGC	ACAAGGTGAA	CCTGAACACC	ATCAAGCGCT	GCCTCCTCAT	CGACTACAAC 660
661	CCCGACTCCC	AGGAGCTGGA	CTTCGCGCAC	TATAGCATCA	AAGTTGTTCC	TGTGGGCGCG 720
721	AGTCGCGGGA	TGAAGAAGCT	GCTCCAGGAG	AAGTTCCCCA	ACATGAGCCG	CCTGCAGGAC 780
781	ATCAGCGAGC	TGCTGGCCAC	GGGCGCGGGG	CTGTCCGAGA	GCGAGGCAGA	GCCTGACGGC 840
841	GACCACAACA	TCACAGAGCT	GCCTCAGGCT	GTGCTGGGCC	GTGGCAACAT	GCGGGCCCCAG 900
901	CAGAGTGCAG	TGCGGCTCAC	CGAGATCGGC	CCGCGGATGA	CAC TGCAGCT	CATCAAGGTC 960
961	CAGGAGGGCG	TCGGGGAGGG	CAAAGTGATG	TTCCACAGTT	TTGTGAGCAA	GACGGAGGAG 1020
1021	GAGCTGCAGG	CCATCCTGGA	AGCCAAGGAG	AAGAAGCTGC	GGCTGAAGGC	TCAGAGGCAG 1080
1081	GCCCAGCAGG	CCCAGAATGT	GCAGCGCAAG	CAGGAGCAGC	GGGAGGCCCA	CAGAAAGGAG 1140
1141	AGCCTGGAGG	GCATGAAGAA	GGCACGGGTC	GGGGGTAGTG	ATGAAGAGGC	CTCTGGGATC 1200
1201	CTTTCAAGGA	CGGCGAGCCT	GGAGTTGGGT	GAGGACGATG	ATGAACAGGA	AGATGATGAC 1260
1261	ATCAGATATT	TCTGCCAGGC	GGTGGGCGAG	GCGCCCACTG	AGGACCTGTT	CCCCGAGGCC 1320
1321	AAGCAGAAAC	GGCTTGCCAA	GTCTCCAGGG	CGGAAGCGGA	AGCGGTGGGA	AATGGATCGA 1380
1381	GGCAGGGGTC	GCCTTTGTGA	CCAGAAGTTT	CCCAAGACCA	AGGACAAGTC	CCAGGGAGCC 1440
1441	CAGGCCAGGC	GGGGGCCAG	AGGGGCTTCC	CGGGATGGTG	GGCGAGGCCG	GGGCCGAGGC 1500
1501	CGCCAGGGGA	AGAGAGTGGC	CTGAGCCCCA	GCCGCACCGG	AGCAGCGGCT	GGATTGAACG 1560
1561	CCCCAGATTG	GGGCCCCAGA	TGTGGCCCTC	GGTTTCCTTT	CATAAAGGAG	TTGTGTCCCC 1620
1621	AGCCCTTCCA	CTCCAGTAAA	GAAGTGAATT	GGCAAAAAAA	AAAA	1664
	10	20	30	40	50	60

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		10		20		30		40		50		60	
1		MGQSGRSRHQ		KRAPFQAQLR		NLEAYAANPH		SFVFTRGCTG		RNIRQLSLDV		RRVMEPV TAS	60
61		RLQVRKKNSL		KDCVAVAGPL		GVTHFLILAK		QETNVYFKLM		RLPGGPTLTF		QVKKYS LVRD	120
121		VVSSLRRHRM		HEQQFAHPPL		LVLNSFGPHG		MHVKLMATMF		QNLFPSINVH		KVNLNTIKRC	180
181		LLIDYNPDSQ		ELDFRHYSIK		VVPVGASRGM		KKLLQEKFPN		MSRLQDISEL		LATGAGLSES	240
241		EAEPDGDHNI		TELPQAVAGR		GNMRAQQSAV		RLTEIGPRMT		LQLIKVQEGV		GEGKVMFH SF	300
301		VSKTEEELQA		ILEAKEKKLR		LKAQRQAQQA		QNVQRKQEQR		EAHRKKSL EG		MKKARVGGSD	360
361		EEASGIPSR T		ASLELGEDDD		EQEDDDIEYF		CQAVGEAPSE		DLPPEAKQKR		LAKSPGRKRK	420
421		RWEMDRGRGR		LCDQKFPKTK		DKSQGAQARR		GPRGASRDGG		RGRGRGRPGK		RVAZ	474
			10		20		30		40		50		60

MM FGQGGKQAAWGSPGGPDIRSAIAPGELRNLESYAAQPHSPV 41
HS

MM FTQG---RAGRNVRQLSLDVRVMEPLTATRLQVRKKNSLKDCVAVAGPLGVTHFLILT 98
HS LGPRVTHTFLILSK 13

MM TD--NSVYLKLMRLPGGPTLTFFQISKYTLIRDVVSLSRRH-RMHEQQFNHPPLVLVNSFG 155
HS TE--INVYFKLMRLPGGPTLTFFQVKKYSLVRODVVSLSRRH-RMHEQQFAHPPLVLVNSFG 70

MM PQG-----MHIKLMATMFQNLFPSINVHTVNLTNIKRCLLINYND-SQELDFRHY 205
HS PHG-----MHVVKLMATMFQNLFPSINVHKVNLTNIKRCSSXDLKPGFPRSLDFRPI 121

MM SVKVVVPVGASRGMKKLLQ-----EKFPNMSRLQDISSELLATGVG----- 244
HS IAFKGGSCWAPNSGGL 137

MM -----LSDSEVEPDGEHN-----TTELPAQAVAG-RGNMQAQQSA 277

MM VRLTEIGPRMTLQLIKIQEGVGNQNVLFHSFVHKTEELQAIIAAKEKRLRLKAQRQHQ 337

MM AENLQRXRSCRXPTRRRAWQA----- 358

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